WHAT IS CLAIMED IS:

Sub (1)

1. A method for determining transcription rate of mRNA in select eukaryotic cells comprising

(a) pausing transcription in the nuclei of select eukaryotic cells containing nascent mRNA transcripts,

(b) incubating said nuclei with labeled nucleoside triphosphate to produce labeled RNA molecules from said nascent mRNA transcripts,

(c) contacting said labeled RNA molecules with an array of at least 500 nucleic acid molecule probes representing at least part of the genome of the native eukaryotic organism for said cells to identify the quantity of nascent mRNA transcripts in said cells.

2. A method according to claim 1 wherein said array comprises oligonucleotides representing part of the transcriptome of said organism.

3. A method according to claim 1 wherein the quantity of at least 100 mRNA transcripts is simultaneously identified.

4. A method according to claim 1 wherein the quantity of at least 500 mRNA transcripts is simultaneously identified.

5. A method according to claim 1 wherein the quantity of at least 1000 mRNA transcripts is simultaneously identified.

6. A method according to claim 1 wherein the quantity of at least 2000 mRNA transcripts is simultaneously identified.

7. A method according to claim 1 wherein the quantity of at least 4000 mRNA transcripts is simultaneously identified.

Sub a2

8. A method for determining a frequency of synthesis for a plurality of mRNA molecules in a eukaryotic cell, said method comprising

(a) pausing transcription in select eukaryotic cells containing nuclei with nascent mRNA transcripts, and

(b) using labeled mRNA transcripts to show a relative rate of synthesis for a plurality of mRNA molecules.

9. A method for determining a rate of degradation for a distinct mRNA molecule in a eukaryotic cell, said method comprising

(c) pausing transcription of mRNA in select eukaryotic cells containing nuclei with nascent mRNA transcripts,

(d) using at least part of said nuclei to determine a frequency of synthesis for a plurality of mRNA transcripts at the time of said pausing:

(e) using at least part of said cells to determine a steady-state level of mRNA at the time of said pausing;

(f) determining relative rates of mRNA degradation for mRNA transcripts by comparing frequencies of synthesis and steady-state concentrations.

10. A method according to claim 9 wherein the rate of degradation is determined simultaneously for at least 100 mRNA molecules.

11. A method according to claim 9 wherein said rate of mRNA degradation is determined for a plurality of related mRNAs by hybridizing said labeled RNA to an array of at least 500 nucleic acid molecules.

12. A method according to claim 11 wherein the rate of mRNA degradation is simultaneously determined for a group of at least 100 related mRNAs.

13. A method for predicting regulatory motifs for transcription rates, comprising:

(1) finding transcription rates of mRNA molecules according to claim 1, and

(2) comparing sequence elements of differentially regulated genes encoding said mRNA molecules to identify regulatory motifs.

14. A method of predicting structural determinants of mRNA stability, comprising:

(1) determining rates of degradation of mRNA molecules according to claim 9, and

(2) comparing gene and mRNA sequence elements of differentially stable mRNAs to identify structural determinants.

15. A method of constructing a recombinant organism with enhanced stability for mRNA transcribed from a gene of interest comprising introducing into the genome of said organism a gene containing at least one sequence element conferring structural stability in an mRNA transcribed from said gene.

16. A method according to claim 15 wherein said sequence element is a structural determinant of mRNA stability predicted by:

(1) determining rates of degradation of mRNA molecules, and

(2) comparing sequence elements of differentially stable mRNAs to identify said structural determinants.